INFORMATION DISCHOBURE					ATTY. DOCKET NO. A-68126-1/RFT/RMS		SERIAL NO. 09/502,984		RECEIVED			
CITATION						APPLICANT PEIZHI et al.				OCT 19 2000		
PTO-1449 CT 1 6				6 2000					UP 1	TECH CENTER 1600/2900		
			PADEMANS. PATENT DO		ENT DOCUMENTS							
EXAMINER'S	s		PATENT NO.	DATE	:			CI.	CLASS SUBCL		FILING DATE	
() 20	-	1	5,292,654.0	03/1994	NAME Yoshimura et al.		CLA	435	SUBCLASS			
7		***										
FOREIGN PATENT DOCUMENTS								-1-4:				
EXAMINER'S INITIALS			PATENT NO.	DATE	COUNTRY			CLASS		SUBCLASS	Yes	slation No
23		2	94/29458	12/1994	PCT							
1		3	98/47089	10/1998	PCT							
	1	4	0 742 438	11/1996	EP							
		5	0 603 8787	02/1994	EP (patent abstracts of Japan)							
			OTHER D	OCUMENT	S (Includi	ing A	Author, Title, Date, P	ertin	ent P	ages, Etc.)		1
()2	OTHER DOCUMENTS (Including Author, Title, Date, Pertinent Pages, Etc.) 6 Dahiyat et al., "Protein design automation," Protein Science, 5:895-903 (1996).											
47		7	Jolliffe et al., "Erythropoietin Receptor: Application in Drug Development," Nephrol. Cial. Transplant., 10(suppl. 2): 28-34 (1995).									
	1	8	Quelle et al., "Mutations in the WSAWSE and Cytosolic Domains of the Erythropoietin Receptor Affect Signal Transduction and Ligand Binding and Internalization," Molecular and Cellular Biology, 12(10): 4553-4561 (1992).									
		9	Barbone et al., "Mutagenesis Studies of the Human Erthropoietin Receptor," The Journal of Biological Chemistry," 272(8): 4985-4992 (1997).									
	1	0	Johnson et al., "Refolding, Purification, and Characterization of Human Erythropoietin Binding Protein Produced in Escherichia coli," Protein Expression and Purification, 7:104-113 (1996).									
	1	1	Livnah et al., "An Antagoisnt Peptide-EPO Receptor Complex Suggests that Receptor Dimerization is not Sufficient for Activation," Nature Structural Biology, 5(11): 993-1003 (1998).									
	1	2	McConnell et al., Isolation of Erythropoietin Recetpor Agonist Peptides Using Evolved Phage Libraries," Biol. Chem., 379:1279-1286 (1998).									
	1	3	Wrighton et al., "Small Peptides as potent Mimetics of the Protein Hormone Erythropoietin," Science, 273:458-463 (1996).									
	1	4			nily Structu	ure	And Biotech Drug De	evelop	omen	it," Biotech	nology, 10:	1529-1534
	1	5	Middleton et al., "Critical Erythropoietin (EPO) Binding Determinanats on the EPO Receptor also Interact," Blood, 88(10): 661A, abstract (1996).									
	1	6	Borman, "Proteins to Order," Chemical and Engineering Newsletter (C&EN) October 6, 1997, 9-10 (1997).									
	17 Lazar et al., "De novo design of the hydrophobic core of ubiquitin," Protein Science 6:1167-1178 (1997).											
18 Desjarlais et al., "New strategies in protein design," Current Opinion in Biotechnology ^:460-466 (1995).							(1995).					
	4	\perp				•		T. F	. /			
EXAMINE	R	1	3 -		·	DA	TE CONSIDERED	/	10	24/0		

XAMINER: Initial if reference considered, whether or not citation is in conformance with MPEP 609; draw line through citation if not in conformance and not considered. clude copy of this form with pext communication to applicant. 8085 1449A.FRM (8/95)

CITATION DISCLOSURE CITATION

PTO-1449 PTO-1449

ATTY. DOCKET NO. A-68126-1/RFT/RMS ERIAL NO. 09/502,984

APPLICANT PEIZHI et al.

FILING DATE
February 11 2000

GROUP

1631 February 11, 2000 OTHER DOCUMENTS (Bicluding Author, Title, Date, Pertinent Pages, Etc.) 19 Wodak, S.J., et al., "Analytical approximation to the accessible surface area of proteins", Proc. Natl. Acad. Sci. USA Vol.77(4):1736-1740 (April 1980). Muñoz, V., et al., "Analysis of the effect of local interactions on protein stability", Folding & Design 1(3):167-178 (April 1996). 21 Dunbrack Jr., R.L., et al., "Conformational analysis of the backbone-dependent rotamer preferences of protein sidechains", Struc. Biol. Vol.1(5):334-340 (May 1994). 22 Hellinga, H.W., et al., "Construction of New Ligand Binding Site in Proteins of Known Structure", J. Mol. Biol. 222:763-785 (1991). Desmet, J., et al., "The Dead End Elimination' Theorem as a New Approach to the Side Chain Packing 23 Protein", from "The Protein Folding Problem and Tertiary Structure Prediction" Ch.10:1-49 (1994). Lasters, I., et al., "Dead-End Based Modeling Tools to Explore the Sequence Space That is Compatible 24 with a Given Scaffold", Jour. of Protein Chem. Vol.16(5):449-452 (July 1997). 25 Sun, S., et al., "Designing amino acid sequences to fold with good hydrophobic cores", Protein Enga. Vol.8(12):1205-1213 (1995). Desmet, J., et al., "The dead-end elimination theorem and its use in protein side-chain positioning", 26 Nature Vol.356:539-542 (April 1992). Bowie, J.U., et al., "Deciphering the Message in Protein Sequences: Tolerance to Amino Acid Substitutions", Science Vol.247:1306-1310 (March 1990). Desjarlais, J.R., et al., "De novo design of the hydrophobic cores of proteins", Protein Science 28 4:2006-2018 (1995). 29 Pabo, C., "Designing proteins and peptides", Nature Vol.301:200 (Jan. 1983). Jones, D.T., "De novo protein design using pairwise potentials and a genetic algorithm", Protein Science 30 3:567-574 (1994). Goldstein, R.F., "Efficient Rotamer Elimination Applied to Protein Side-Chains and Related Spin Glasses", Biophys. Jour. Vol.66:1335-1340 (May 1994). Mayo et al., "First fully automatic design of a protein achieved by Caltech scientists", new press 32 release (Oct. 1997). 33 Smith, C.K., et al., "Guidelines for Protein Design: The Energetics of β Sheet Side Chain Interactions" Science Vol.270:980-982 (Nov. 1995). Regan, L., "Helix is a helix?", Proc. Natl. Acad. Sci. USA Vol.94:2796-2797 (April 1997). 34 Muñoz, V., et al., "Intrinsic Secondary Structure Propensities of the Amino Acids, Using Statistical φ-35 ψ Matrices: Comparison with Experimental Scales", Proteins 20:301-311 (1994). 36 Stickle et al., "Bydrogen Bonding in Globular Proteins," Journal of Molecular Biology, 226:1143-1159 (1992).Lasters et al., "Enhanced dead-end elimination in the search for the global minimum energy 37 conformation of a collection of protein chains," Protein Engineering, 8(8):815-822 (1995). 38 Desmet et al., "Theoretical and Algorithmical Optimization of the Dead-End Elimination Theorem," Proceedings of the Pacific Symposium on Biocomputing '97, 122-133 (1997). Holmes, "First-ever designer protein fits like a glove," New Scientist, IPC Magazines Limited, 11 October 39 1997 (1997) **EXAMINER** DATE CONSIDERED

XAMINER: Initial if reference considered, whether or not citation is in conformance with MPEP 609; draw line through citation if not in conformance and ot considered. Include copy of this form with next communication to applicant. 8085 1449A.FRM (8/95)

INFORMATION DISCLOSURE
CITATION OUT 1 6 2000
PTO-1449

ATTY. DOCKET NO. A-68126-1/RFT/RMS

ERIAL NO. 09/502,984

APPLICANT PEIZHI et al.

FILING DATE February 11, 2000 | 1631

GROUP

		February 11, 2000 1031							
		OTHER DOCUMENTS (Including Author, Title, Date, Pertinent Pages, Etc.)							
93	40	Muñoz, V., et al., "Helix design, prediction and stability", <i>Curr. Opin. in Biotech.</i> 6:382-386 (Aug. 1995).							
Minor Jr., D.L., "Measurement of the β-sheet-forming propensities of amino acids", Natural Vol.367:660-663 (Feb. 1994).									
	42	Hellinga, H.W., et al., "Optimal sequence selection in proteins of known structure by simulated evolution", <i>Proc. Natl. Acad. Sci., USA</i> Vol.91:5803-5807 (June 1994).							
	43	Bowie, J.U., et al., "A Method to Identify Protein Sequences that Fold into a Known Three- Dimensional Structure", Science Vol.253:164-170 (July 1991).							
	44	Dalal, S., et al., "Protein alchemy: Changing β -sheet into α -helix", <i>Nature Struc. Biol.</i> Vol.4(7):548-552 (July 1997).							
	45	Dahiyat, B.I., et al., "Proteins from Scratch", press digest email by Science (Sep. 26, 1997).							
	46	Berry, A., et al., "A quantitative methodology for the de novo design of proteins", <i>Protein Sci.</i> 3:1871-1882 (Oct. 1994).							
	47	Hellinga, H.W., "Rational protein design: Combining theory and experiment", <i>Proc. Natl. Acad. Sci, USA</i> Vol.94:10015-10017 (Sept. 1997).							
	48	Padmanabhan, S., et al., "Relative helix-forming tendencies of nonpolar amino acids", <i>Nature</i> Vol.344:268-270 (March 1990).							
	49	Connolly, M.L., "Solvent-Accessible Surfaces of Proteins and Nucleic Acids", Science Vol.221(4612):709-713 (Aug. 1983).							
	50	Eisenberg, D., et al., "Solvation energy in protein folding and binding", <i>Nature</i> Vol.319:199-203 (Jai 1986).							
	 Ponder, J.W., et al., "Use of Packing Criteria in the Enumeration of Allowed Sequences for Structural Classes", release by <i>Acad. Press Inc. (London) Ltd.</i> pp.775-791(1987). Dahiyat, B.I., et al., "Automated design of the surface positions of protein helices", <i>Protein</i> 6:1-5 (June 1997). Harbury et al., "High-Resolution Protein Design with Backbone Freedom," <i>Science</i>, 282:1462-146 								
	54	Kortemme et al., "Design of a 20-Amino Acid, Three-Stranded β-Sheet Protein," <i>Science</i> , 281:253-256 (1998).							
Koehl et al., "De Novo Protein Design. I. In Search of Stability and Specificity," J. Mol. Biol., 293:1 (1999).									
	,								
EXAMINER		DATE CONSIDERED / 24/01							

XAMINER: Initial if reference considered, whether or not citation is in conformance with MPEP 609; draw line through citation if not in conformance and ot considered. Include copy of this form with next communication to applicant. 085 1449A.FRM (8/95)

INFORMATION DISCLOSURE CITATION PTO-1449 ATTY. DOCKET NO.
A-68126-1/RFT/RMS

O9/502,984

RECEIVED

APPLICANT PEIZHI et al.

OCT 19 2000

FILING DATE February 11, 2000

GROUP 1631 TECH CENTER 1600/2300

		P10-1449		February 11, 2000	1631	1600/2900			
		OTHER DOCUMENTS WELL	ling	Author, Title, Date, Prtir	ent Pages,	Etc.)			
12/	56	Gordon et al. "Energy functions for protein design," Curr. Opinion in Struct. Biol., 9:509-513 (1999).							
0,0	57	Cornell et al., "A Second Generation Force Field for the Simulation of Proteins, Nucleic Acids, and Organic Molecules," <i>J. Am. Chem. Soc.</i> , 117:5179-5197 (1995).							
	 Villegas et al., "Stabilization of proteins by rational design of α-helix stability using helix/coil transit Folding & Design, 1(1):29-34 (1995). Hurley et al., "Design and Structural Analysis of Alternative Hydrophobic Core Packing Arrangeme Bacteriophage T4 Lysozyme," J. Mol. Biol., 224:1143-1159(1992). 								
	60	Tuffery et al., "A New Approach to t Biomolecular Struct. & Dynamics, s		f Protein Side Chain Conformations," J. of					
	61	Brooks et al., "CHARMM: A Program for Macromolecular Energy, Minimization, and Dynamics Calculations," <i>J. of Computational Chemistry</i> , 4(2):187-217 (1983).							
	62	Rappé et al., "Charge Equilibration (1991).	tions," <i>J. Ph</i>	ys. Chem., 95:3358-3363					
	63	Mayo et al., "DREIDING: A Generic Force Field for Molecular Simulations," <i>J. Phys. Chem.</i> , 94:8897-8909 (1990).							
	64	Harbury et al., "Repacking protein cores with backbone freedom: Structure prediction for coiled coils," <i>Proc. Natl. Acad. Sci. USA</i> , 92:8408-8412 (1995).							
	65	Kono et al., "Energy Minimization Method Using Automata Network for Sequence and Side-Chain Conformation Prediction from Given Backbone Geometry," <i>Proteins: Structure, Function, and Genetics</i> , 19:244-255 (1994).							
	66	Lee et al., "Accurate prediction of the stability and activity effects of site-directed mutagenesis on a protein core," <i>Nature</i> , 352:448-451 (1991).							
	67	van Gunsteren et al., "Prediction of the Activity and Stability Effects of Site-directed Mutagenesis on a Protein Core," <i>J. Mol. Biol.</i> , 227:389-395 (1992).							
	68	Wesson et al., "Atomic solvation parameters applied to molecular dynamics of proteins in solution," <i>Protein Science</i> , 1:227-235 (1992).							
	69	Dahiyat et al., "Protein design automation," Caltech Biology Annual Report, 172 (1995).							
	70	Dahiyat et al., "Probing the Role of Specificity in Protein Design," <i>Caltech Biology Annual Report</i> , 160-161 (1996).							
	71	DeGrado, W., "Proteins from Scratch," Science, 278:80-81 (1997).							
72 Dahiyat et al., "De Novo Protein Design: Fully Automated Sequence Selection," Science, 27									
	73 Dahiyat et al., "Protein Design Automation," Meeting Abstract; Protein Science Vol. 4, Suppl. 2, 83 (1)								
4	74	Dahiyat et al., "Protein design Autor	mati	ion," Poster Sessions, Prote	in Science '	Vol.5, Suppl. 1, 22-23 (1996)			
EXAMINER		2 ~	D	ATE CONSIDERED	1 1	4/01			

XAMINER: Initial if reference considered, whether or not citation is in conformance with MPEP 609; draw line through citation if not in conformance and not onsidered. Include copy of this form with next communication to applicant.

085 1449A.FRM (8/95)1024004